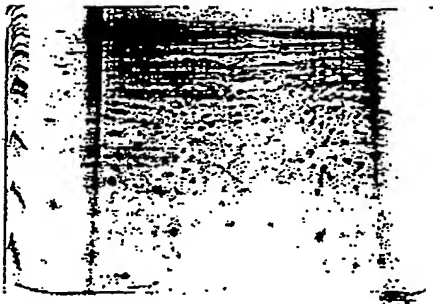
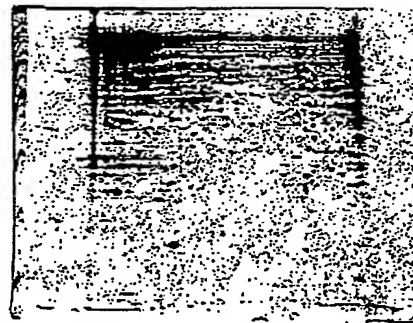


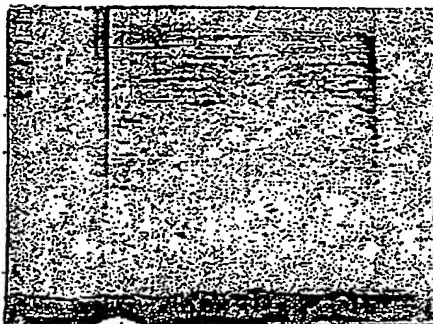
Figure 1



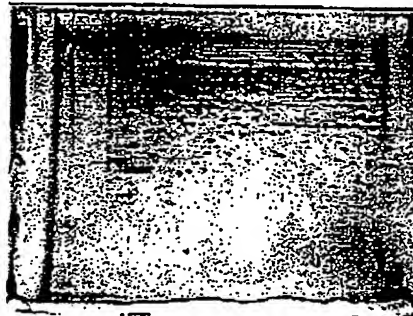
Hochstrasser: 8100 ng



Amersham Biosciences: 8100 ng

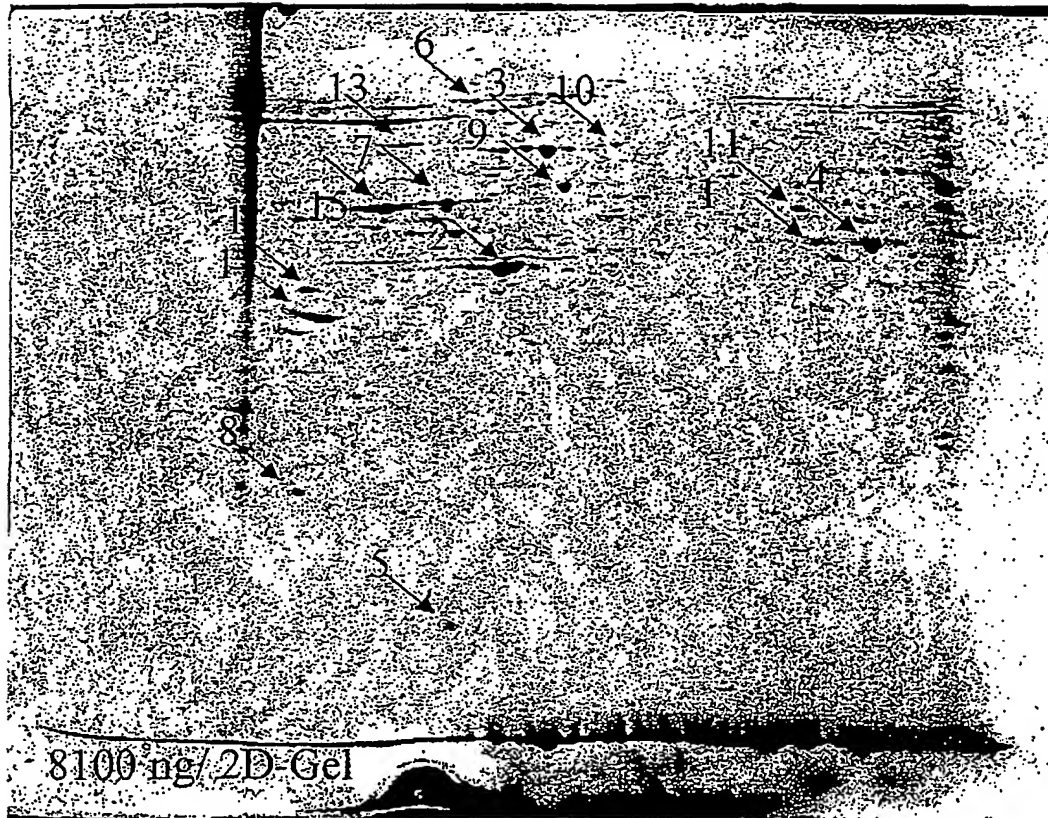


SYPRO Ruby: 8100 ng



Novel silver staining: 300 ng

Figure 2



3/6

Figure 3

Spot No.	Colloidal Coomassie	Novel silver staining	Hoch- strasser	Amersham Biosciences
1	11	7	9	4
2	22	22	18	20
3	21	31	13	19
4	35	38	4	9
5	-	-	-	-
6	18	22	3	3
7	24	24	11	11
8	15	8	0	8
9	8	15	3	7
10	14	14	0	3
11	5	11	2	0
12	(~4)	(~4)	(~4)	(~4)
13	9	11	2	9
14	23	25	11	15
15	(~13)	(~13)	(~13)	(~3)
Average	17.1	19.0	6.3	9.0

Figure 4A

Spot	Name	Peptide sequence
1	Nucleophosmin	Peptides unsuitable for sequencing
2	Actin (isoform n.d.)	AVFPSIVGR GYSPTTAAER SYELPDQCVITIGNER VAPECHFVLLTAPLEPK
3	Heat shock protein cognate 70	DAGTIAGLNLVLR TVTNNAVTVPAYFNDQR SINPDEAVAYQAAVQAAILSCDK QTQTFTTYSNQPGVLIQVYEGER
4	Enolase 1, alpha non neuron	GNPTVEVCLYAK YITPDQLADLYK AAVPSGASTGIYEALER
5	no name, keratin contamination	
6	Heat shock protein 110 kDa	VLATAFDITLGGK AGGIETIANEYSQR ELSTTLNADEAVTR EPSITDVVPYPISLR
7	Tubulin alpha 5	KIIDLVLDR AVFVDLEPTVIDEVR VGINYQPPTVVPGDLAK TIGGGDDSPNTFFSETGAGK
8	tumor protein; translationally controlled 1 (21 kDa)	EIADGLCLEVEGR Cye_CAM
9	Chaperonin groEL precursor	TLNDELEIIEGMK CEPQDAYVLLSEK AAVEEGIVLGGCALLR YSSVQSIVPALEIANAKR
10	heat shock protein 74 kDa	VQQTVDLFR SDIGEVILVGGMTR Mox LLGQPTFLIGIPPAPR NAVITVPAYFNDQR
11	Chaperonin subunit 2 (beta)	QVLLSAAEAARVILR EALLSSAVDHGSDAR
12	Enolase 1, 2, or 3 (alpha, beta, or gamma)	AAVPSGASTGIYEALER
13	dnak-type molecular chaperone grp78 precursor	ITPSTVAPTPEGER VTHAVVTVPAYFNDQR DNHLLGTFDLTGIPPAPR
14	Lamin receptor 1; p40-3, functional ; p40-8, functional	FAAATGATPIAGR YVDIALPCMK FTPGTFTWQIAAFR ATVAIENPADVSIISSR
15	tubulin (beta 2, 3 or 5 or mixture)	YLTVAAVFR PGQLNADLR ISEQFTAMPR ISEQFTAMPR Mox
		Possible score 4200

Figure 4B

Novel method	%	Colloidal Coomassie	%	Spot
				1
NH2-AVFPSSIVGR-COOH	100	NH2-AVFPSSIVGR-COOH	100	2
NH2-GYSFTTT...-COOH	70	NH2-GYSFTTT...-COOH	70	
NH2-SYELPDGQVITIGNER-COOH	100	NH2-SYELPDGQVITIGNER-COOH	100	
	0	NH2-...FVLLTEAPLNPK-COOH	67	
NH2-DAGTIA...-COOH	46	NH2-DAGTIAGLNLNR-COOH	92	3
NH2-...VVTV...-COOH	22	NH2-TVTNAVTVPAYFNDQR-COOH	100	
NH2-SINPDEAVAYGAAVQAAILSGDK-COOH	100	NH2-SINPDEAVAYGAAVQAAILSGDX-COOH	100	
	0	NH2-...PGVLIQVVEGR-COOH	50	
NH2-GNPTVEVDLYTAK-COOH	100	NH2-GNPTVEVDLYTAK-COOH	100	4
NH2-YTFPDQLADLYK-COOH	100	NH2-YTFPDQLADLYK-COOH	100	
NH2-AAVPSGASTGIYEALER-COOH	100	NH2-AAVPSGASTGIYEALER-COOH	100	
				5
NH2-VLATAPDTT...-COOH	69	NH2-VLATAPDTT...-COOH	54	6
NH2-...ETIA...-COOH	29	NH2-...ETIA...-COOH	29	
NH2-ELSTTLNADAVTR-COOH	100	NH2-...TTLANA...-COOH	16	
NH2-EFSITDVV...-COOH	87		0	
NH2-EIIDLVLDR-COOH	100	NH2-EIIDLVLDR-COOH	100	7
NH2-AVFDLEPTVIDEVR-COOH	100	NH2-AVFDLEPTVIDEVR-COOH	100	
NH2-...YQPPFVV...AK-COOH	50	NH2-...YQPPFVV...-COOH	44	
NH2-...DSFNTFFSETGAGK -COOH	70	NH2-...DSFNTFFSETGAGK -COOH	70	
NH2-EIADGLCLEV...-COOH	77	NH2-EIADGLCLEVEGK-COOH	100	8
NH2-TLNDELEIIEGMK-COOH	100	NH2-TLNDELEIIEGMK-COOH	100	9
NH2-CBFQDAYVLLSEK -COOH	100	NH2-CBFQDAYVLLSEK -COOH	100	
NH2-...EEGIVLGGGCALLR-COOH	82	NH2-...EEGIVLGGGCALLR-COOH	82	
NH2-...QSIHPALEIA...R-COOH	61	NH2-...SIVPALEIA...R-COOH	56	
NH2-VQQTVDL...-COOH	73	NH2-VQQTVDL...-COOH	73	10
NH2-...VILVG...-COOH Max	36	NH2-...VILVG...-COOH Max	36	
	0	NH2-...FTLI...-COOH	27	
NH2-...TV...QR-COOH	27	NH2-...TV...QR-COOH	27	
NH2-QVLSAAEA...-COOH	60		0	11
NH2-...DHGSD...-COOH	31			
NH2-...PSGASTGI...-COOH	44	NH2-...PSGASTGI...-COOH	44	12
NH2-ITPSYVAPT...-COOH	64		0	13
NH2-...VVTVPAYF...-COOH	47			
NH2-...TQXP...-COOH	22			
NH2-FAAATGAT...-COOH	62	NH2-FAAATGAT...-COOH	62	14
NH2-YVDIAIPCNNK -COOH	100	NH2-YVDIAIPCNNK -COOH	100	
NH2-FTPGTFINQIAAFR -COOH	100	NH2-FTPGTFINQIAAFR -COOH	100	
NH2-AIVAIENPADSVIISR-COOH	100	NH2-AIVAIENPADSVIISR-COOH	100	
NH2-YLTVAAVFR-COOH	100	NH2-YLTVAAVFR-COOH	100	15
NH2-ISEQFT...R-COOH	0	NH2-PGQLNADLR -COOH	100	
NH2-ISEQFTAMFR-COOH	70	NH2-ISEQFTAMFR-COOH	100	
	100	NH2-ISEQFTAMFR-COOH	100	
Score achieved:	2799		2819	
Percentage of possible score:	67		67	

Figure 4C

Hochstrasser	%	Amerham Biosciences	%	Spot
				1
NH2-AVFPSIVGR-COOH	100	NH2-AVFPSIVGR-COOH	100	2
NH2-CYSFTT...-COOH	70	NH2-GYSFTT...-COOH	70	
NH2-SYELPDGQVITIGNR-COOH	100	NH2-SYELPDGQVITIGNR-COOH	100	
NH2-...PVLLTEAPLAPK-COOH	67	NH2-...PVLLTEAPLAPK-COOH	67	
NH2-...IA...-COOH	15	NH2-QACTIASLNVLK-COOH	92	3
NH2-...VVTV...-COOH	22	NH2-...VVTV...-COOH	22	
	0	NH2-SINPDEAVYCAAVQAATLSGDK-COOH	100	
	0	NH2-...PGVLIQVY...-COOH	33	
NH2-...V2...-COOH	15	NH2-GNPTVEVDLY...-COOH	77	4
NH2-YITP...-COOH	33	NH2-YITPDQLADLYK-COOH	100	
NH2-AAVPSGASTGIYEALR-COOH	100	NH2-AAVPSGASTGIYEALR-COOH	100	
				5
NH2-...-COOH	0	NH2-...-COOH		6
NH2-...ETI...-COOH	21	NH2-...-COOH		
NH2-...-COOH	0	NH2-...-COOH		
NH2-...TDVV...-COOH	27	NH2-...-COOH		
NH2-EIIDLVLDR-COOH	100	NH2-EIIDLVLDR-COOH	100	7
NH2-AVFVDLEPTVIDSVK-COOH	100	NH2-...VDLEPTVI...-COOH	53	
	0		0	
	0		0	
----	0		0	8
	0		0	9
NH2-...EGIVLGGCALLR-COOH Cys_CAM	76	NH2-...ECIVLOG...-COOH	41	
	0		0	
	0		0	
	0		0	10
NH2-QVLSAAEA...-COOH	60			11
NH2-...PSGASTGI...-COOH	44	NH2-...PSGASTGI...-COOH	44	12
				13
NH2-PTPGTPTNQIAAFK-COOH	0		0	14
NH2-AIVAIENPADVSVISR-COOH	100		0	
	100	NH2-...AIENP...-COOH	29	
NH2-YLTVAAVFR-COOH	100	NH2-YLTVAAVFR-COOH	100	15
NH2-PGQLNADLR-COOH	100	NH2-PGQLNADLR-COOH	100	
NH2-ISEQPT...R-COOH	70	NH2-ISEQPTA...R-COOH	80	
NH2-ISEQF...R-COOH	60	NH2-ISEQF...R-COOH	60	
	1480		1468	
	35		35	